

Figure 1A

Figure 1B

ATCTGGACCAGGCTGTGGGTAGATGTCAATAGAAATAGCTAATTATTCCTCCANGTGTGCTTAAGCGTGGCTG 1169
ACCAGGCTTCTTCCTACATCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGCATTGTCAG 1248
CTCCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGTCTGGAGACTCAGGCAGGGTAAACTGCAGGAGCAGTTGC 1327
CACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTGGCAGACAGCCGTTGTTCTACATGGCTTGATAATTG 1406
TTTGAGGGGAGGAGATGGAACAAATGTGGAGTCTCCCTCTGATTGGTTTGGGAAATGTGGAGAAGAGTGCCCTGCTT 1485
TGCAAACATCAACCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCATGGCATAGGTAAGCTGTGCCT 1564
TCAGCTGTTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCCAGCAGTGTGCTCAGCTCCTAC 1643
CTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTCCCTCTCAGCACAGCCTGGGAGGGGTCATTGTTCTC 1722
CTCGTCATCAGGGATTCAGAGGCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAG 1801
TTTCATCTGGTTGTGACTCTAAGCTCAGTGCCTCTCCACTACCCACACCAGCCTGGTGCCACAAAAGTGCCTCCC 1880
AAAAGGAAGGAGAATGGGATTTCAGGGATTCAGGGCATGCACATCTGAATTAAAGGTCAAACAAATTCTCACATCCCTCTA 1959
AAAGTAAACTACTGTTAGAACAGCAGTGTCTCACAGTGTGGGCAGCCGTCTTAATGAAGACAATGATATTGAC 2038
ACTGTCCTCTTGGCAGTTGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAA 2117
CAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAAACTACTAGCAGCAACTGAAGACAATTATCA 2196
ACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACACTCTACG 2275
CCACTCCACAAATGATTTTCAGGTGTCATGGACTGTTGCCACCATGTATTCCAGAGTTCTAAAGTTAAAGTT 2354
GCACATGATTGTATAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGCATAA 2433
ATCACTTCAACTGCTAAAAAAAAAAAAAAAAAAAAAA 2479

Figure 2

GAATTCTGGCACGAGAGACGACGTGCTGAGCTGCCAGCTTAGTGGAAAGCTCTGCTCTGGGTGGAGAGCAGCCTCGCTTTG	79
M V A A V L L G	8
GTGACGCACAGTGCTGGGACCCCTCCAGGAGCCCCGGATTGAAGG ATG GTG GCG GCC GTC CTG CTG GGG	148
L S W L C S P L G A L V L D F N N I R S	28
CTG AGC TGG CTC TGC TCT CCC CTG GGA GCT CTG GTC CTG GAC TTC AAC AAC ATC AGG AGC	208
S A D L H G A R K G S Q C L S D T D C N	48
TCT GCT GAC CTG CAT GGG GCC CGG AAG GGC TCA CAG TGC CTG TCT GAC ACG GAC TGC AAT	268
T R K F C L Q P R D E K P F C A T C R G	68
ACC AGA AAG TTC TGC CTC CAG CCC CGC GAT GAG AAG CCG TTC TGT GCT ACA TGT CGT GGG	328
L R R R C Q R D A M C C P G T L C V N D	88
TTG CGG AGG AGG TGC CAG CGA GAT GCC ATG TGC TGC CCT GGG ACA CTC TGT GTG AAC GAT	388
V C T T M E D A T P I L E R Q L D E Q D	108
GTT TGT ACT ACG ATG GAA GAT GCA ACC CCA ATA TTA GAA AGG CAG CTT GAT GAG CAA GAT	448
G T H A E G T T G H P V Q E N Q P K R K	128
GGC ACA CAT GCA GAA GGA ACA ACT GGG CAC CCA GTC CAG GAA AAC CAA CCC AAA AGG AAG	508
P S I K K S Q G R K G Q E G E S C L R T	148
CCA AGT ATT AAG AAA TCA CAA GGC AGG AAG GGA CAA GAG GGA GAA AGT TGT CTG AGA ACT	568
F D C G P G L C C A R H F W T K I C K P	168
TTT GAC TGT GGC CCT GGA CTT TGC TGT GCT CGT CAT TTT TGG ACG AAA ATT TGT AAG CCA	628
V L L E G Q V C S R R G H K D T A Q A P	188
GTC CTT TTG GAG GGA CAG GTC TGC TCC AGA AGA GGG CAT AAA GAC ACT GCT CAA GCT CCA	688
E I F Q R C D C G P G L L C R S Q L T S	208
GAA ATC TTC CAG CGT TGC GAC TGT GGC CCT GGA CTA CTG TGT CGA AGC CAA TTG ACC AGC	748
N R Q H A R L R V C Q K I E K L *	225
AAT CGG CAG CAT GCT CGA TTA AGA GTA TGC CAA AAA ATA GAA AAG CTA TAA	799
ATATTTCAAAATAAAGAAGAACATCCACATTGCAAAAAAAAAAAAAAAA	848

Figure 3

GTCGACCCACCGTCCGGACCGTGGCGGCACGGTTCTGGGGACCCAGGCTGCAAAGTGACGGTCATTTCTC 79

M	M	A	L	G	A	A	G	A	T	R	V	12								
TTT	CTT	CCT	CTT	GAG	ATG	ATG	GCT	CTG	GGC	GCA	GCG	GGA	GCT	ACC	CGG	GTC	144			
F	V	A	M	V	A	A	L	G	G	H	P	L	L	G	V	S	A	T	32	
TTT	GTC	GCG	ATG	GTA	GCG	GCG	GCT	CTC	GGC	GGC	CAC	CCT	CTG	CTG	GGG	GTG	AGC	GCC	ACC	204
L	N	S	V	L	N	S	N	A	I	K	N	L	P	P	P	L	G	G	A	52
TTG	AAC	TCG	GTT	CTC	AAT	TCC	AAC	GCT	ATC	AAG	AAC	CTG	CCC	CCA	CCG	CTG	GGC	GGC	GCT	264
A	G	H	P	G	S	A	V	S	A	A	P	G	I	L	Y	P	G	G	N	72
GCG	GGG	CAC	CCA	GGC	TCT	GCA	GTC	AGC	GCC	GGC	CCG	GGG	ATC	CTG	TAC	CCG	GGC	GGG	AAT	324
K	Y	Q	T	I	D	N	Y	Q	P	Y	P	C	A	E	D	E	E	C	G	92
AAG	TAC	CAG	ACC	ATT	GAC	AAC	TAC	CAG	CCG	TAC	CCG	TGC	GCA	GAG	GAC	GAG	GAG	TGC	GGC	384
T	D	E	Y	C	A	S	P	T	R	G	G	D	A	G	V	Q	I	C	L	112
ACT	GAT	GAG	TAC	TGC	GCT	AGT	CCC	ACC	CGC	GGG	GAC	GCA	GGC	GTG	CAA	ATC	TGT	CTC	444	
A	C	R	K	R	R	K	R	C	M	R	H	A	M	C	C	P	G	N	Y	132
GCC	TGC	AGG	AAG	CGC	CGA	AAA	CGC	TGC	ATG	CGT	CAC	GCT	ATG	TGC	TGC	CCC	GGG	AAT	TAC	504
C	K	N	G	I	C	V	S	S	D	Q	N	H	F	R	G	E	I	E	E	152
TGC	AAA	AAT	GGA	ATA	TGT	GTG	TCT	TCT	GAT	CAA	AAT	CAT	TTC	CGA	GGG	GAA	ATT	GAG	GAA	564
T	I	T	E	S	F	G	N	D	H	S	T	L	D	G	Y	S	R	R	T	172
ACC	ATC	ACT	GAA	AGC	TTT	GGT	AAT	GAT	CAT	AGC	ACC	TTG	GAT	GGG	TAT	TCC	AGA	AGA	ACC	624
T	L	S	S	K	M	Y	H	T	K	G	Q	E	G	S	V	C	L	R	S	192
ACC	TTG	TCT	TCA	AAA	ATG	TAT	CAC	ACC	AAA	GGG	CAA	GAA	GGT	TCT	GTT	TGT	CTC	CGG	TCA	684
S	D	C	A	S	G	L	C	C	A	R	H	F	W	S	K	I	C	K	P	212
TCA	GAC	TGT	GCC	TCA	GGG	TTG	TGT	TGT	GCT	AGA	CAC	TTC	TGG	TCC	AAG	ATC	TGT	AAA	CCT	744
V	L	K	E	G	Q	V	C	T	K	H	R	R	K	G	S	H	G	L	E	232
GTC	CTG	AAA	GAA	GGT	CAA	GTG	TGT	ACC	AAG	CAT	AGG	AGA	AAA	GGC	TCT	CAT	GGA	CTA	GAA	804
I	F	Q	R	C	Y	C	G	E	G	L	S	C	R	I	Q	K	D	H	H	252
ATA	TTC	CAG	CGT	TGT	TAC	TGT	GGG	GAA	GGT	CTG	TCT	TGC	CGG	ATA	CAG	AAA	GAT	CAC	CAT	864
Q	A	S	N	S	S	R	L	H	T	C	Q	R	H	*						267
CAA	GCC	AGT	AAT	TCT	TCT	AGG	CTT	CAC	ACT	TGT	CAG	AGA	CAC	TAA						909
ACCAGCTATCCAAATGCAGTGAACCTCTTTATATAATAGATGCTATGAAACCTTTATGACCTTCATCAACTCAATC	988																			
CTAAGGATATACAAGTTCTGTGGTTTCAGTTAACGATTCCAATAACACCTTCAAAAACCTGGAGTGTAAAGAGCTTGT	1067																			
TTCTTATGAACTCCCCGTGATTGCAGTAAATTACTGTATTGTAATTCTCAGTGTGGCCTTACCTGTAAATGCAA	1146																			
TGAAACTTTAATTATTTCTAAAGGTGCTGACTGCCTATTTCTCTTGTTATGTAATTCTTACACATTGAT	1225																			
TGTTATCTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTCAGCTTATAGTCTTAAAGCATAACCCTT	1304																			
TACCCCATTAATTCTAGAGTCTAGAACGCAAGGATCTTGGAAATGACAAATGATAGGTACCTAAAATGTAACATGAA	1383																			
AATACTAGCTTATTCTGAAATGTAATCTTAAATGCTTAAATTATTTCCTTAGGCTGTGATAGTTTGAAAT	1462																			
AAAATTAACATTTAATATCATGAAATGTTAAGTAGACATAAAAAAAAAAGGGCGGCCGC	1536																			

Figure 4A

GTCGACCCACCGTCCGGCGGGAGCCCGCGCGAGCGTAGCGCAAGTCGCTCCCTAGGCATCGCTGCCTGGCAGCGA 79
 TTGCTGTCTCTTGAGTCAGGGACAACGCTCGGGGCAACTGTGAGTGCAGCTGTGGGGACCTGATTCTCTCA 158
 GATCTCGAGGATTGGTCCGGGACGTCTCCTGATCCCCTACTAAAGCGCTGCTAACCTTGAAAAGGAGCACTGTGTC 237
 CTGAAAGTTGACACATAAAGGATAGGAAAAGAGAGGAGAGAAAAGCAACTGAGTTGAAGGAGAAGGAGCTGATGCC 316
 GCCTCTGATCAATTAAGAGGAGAGTTAACCGCCGAGATCCGGCGGGACCAAGGAGGTGCGGGCAAGAAGGAACGG 395
 AAGCGGTGCGATCCACAGGGCTGGGTTTCTTGCACCTGGTCACGCCCTGGCGAGAAAGCGCTCGCATTGAT 474
 TGCTTCCAGTTATTGAGAAGCTTCTGTCTGGTGGAGAACGGGCTCGCTTGGGCTCGCTAACCTTGAGG 553
 CGTGAGACTGAGTTCATAGGTCTGGTCCCCGAACCAGGAAGGGTTGAGGAAACACAATCTGCAAGCCCCCGGAC 632
 CAAAGTGAGGGGCCCGTGTGGGTCCTCCCTTGCATTCCCACCCCTCCGGCTTGCCTGGGACCC 711

	M	A	A	L	M	R	S	K	D	S	S	C	C	L	L	L	L	17			
	CCTCGCCGGGAG	ATG	GCC	GCG	TTG	ATG	CGG	AGC	AAG	GAT	TCG	TCC	TGC	TGC	CTG	CTC	CTA	CTG	774		
	A	A	V	L	M	V	E	S	S	Q	I	G	S	S	R	A	K	L	N	S	37
	GCC	GCG	GTG	CTG	ATG	GTG	GAG	AGC	TCA	CAG	ATC	GGC	AGT	TCG	CGG	GCC	AAA	CTC	AAC	TCC	834
	I	K	S	S	L	G	G	E	T	P	G	Q	A	A	N	R	S	A	G	M	57
	ATC	AAG	TCC	TCT	CTG	GGC	GGG	GAG	ACG	CCT	GGT	CAG	GCC	AAT	CGA	TCT	GCG	GGC	ATG	ATG	894
	Y	Q	G	L	A	F	G	G	S	K	K	G	K	N	L	G	Q	A	Y	P	77
	TAC	CAA	GGA	CTG	GCA	TTC	GGC	GGC	AGT	AAG	AAG	GGC	AAA	AAC	CTG	GGG	CAG	GCC	TAC	CCT	954
	C	S	S	D	K	E	C	E	V	G	R	Y	C	H	S	P	H	Q	G	S	97
	TGT	AGC	AGT	GAT	AAG	GAG	TGT	GAA	GTT	GGG	AGG	TAT	TGC	CAC	AGT	CCC	CAC	CAA	GGA	TCA	1014
	S	A	C	M	V	C	R	R	K	K	K	R	C	H	R	D	G	M	C	C	117
	TCG	GCC	TGC	ATG	GTG	TGT	CGG	AGA	AAA	AAG	AAG	CGC	TGC	CAC	CGA	GAT	GGC	ATG	TGC	TGC	1074
	P	S	T	R	C	N	N	G	I	C	I	P	V	T	E	S	I	L	T	P	137
	CCC	AGT	ACC	CGC	TGC	AAT	AAT	GGC	ATC	TGT	ATC	CCA	GTT	ACT	GAA	AGC	ATC	TTA	ACC	CCT	1134
	H	I	P	A	L	D	G	T	R	H	R	D	R	N	H	G	H	Y	S	N	157
	CAC	ATC	CCG	GCT	CTG	GAT	GGT	ACT	CGG	CAC	AGA	GAT	CGA	AAC	CAC	GGT	CAT	TAC	TCA	AAC	1194
	H	D	L	G	W	Q	N	L	G	R	P	H	T	K	M	S	H	I	K	G	177
	CAT	GAC	TTG	GGA	TGG	CAG	AAT	CTA	GGG	AGA	CCA	CAC	ACT	AAG	ATG	TCA	CAT	ATA	AAA	GGG	1254
	H	E	G	D	P	C	L	R	S	S	D	C	I	E	G	F	C	C	A	R	197
	CAT	GAA	GGA	GAC	CCC	TGC	CTA	CGA	TCA	TCA	GAC	TGC	ATT	GAA	GGG	TTT	TGC	TGT	GCT	CGT	1314
	H	F	W	T	K	I	C	K	P	V	L	H	Q	G	E	V	C	T	K	Q	217
	CAT	TTC	TGG	ACC	AAA	ATC	TGC	AAA	CCA	GTG	CTC	CAT	CAG	GGG	GAA	GTC	TGT	ACC	AAA	CAA	1374
	R	K	K	G	S	H	G	L	E	I	F	Q	R	C	D	C	A	K	G	L	237
	CGC	AAG	AAG	GGT	TCT	CAT	GGG	CTG	GAA	ATT	TTC	CAG	CGT	TGC	GAC	TGT	GCG	AAG	GGC	CTG	1434
	S	C	K	V	W	K	D	A	T	Y	S	S	K	A	R	L	H	V	C	Q	257
	TCT	TGC	AAA	GTA	TGG	AAA	GAT	GCC	ACC	TAC	TCC	TCC	AAA	GCC	AGA	CTC	CAT	GTG	TGT	CAG	1494
	K	I	*	260																	
	AAA	ATT	TGA	1503																	
	TCACCATGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTAATGCATTAGCATGGTGGAAAAATAAGGTT 1582																				
	CAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAAAAGGGAGAAAGAAAATGAC 1661																				
	TGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATGCAACTTGTCTATGAAATAATGTACAC 1740																				

Figure 4B

ATTTGTGGAAAATGCTATTATAAGAGAACAGCACACAGTGGAAATTACTGATGAGTAGCATGTGACTTTCCAAGAGT 1819
TTAGGTTGTGCTGGAGGAGGGTTCCCTCAGATTGCTGATTGCTTACAAATAACCTACATGCCAGATTCTATTCA 1898
ACGTTAGAGTTAACAAAATCTCTAGAATAACTTGTATACAATAGTTCTAAAATAAAATTGCTAACAGAAAT 1977
GAAAACATGGAGCATTGTTAATTACAACAGAAAATTACCTTTGATTGTAACACTACTTCTGCTGTTCAATCAAGAG 2056
TCTTGGTAGATAAGAAAAAAATCAGTCATAATTCCAAATAATTGCAAATAATGCCAGTTGTTAGGAAGGCCTTA 2135
GGAAGACAAATAACAAACAGCCACAAATACTTTTCAAATTTAGTTTACCTGTAATTAAAGAA 2214
CTGATACAAGACAAAAACAGTCCTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTC 2293
TGAATGCATTATATTCCAAAGTATAACCCATAATTGTGACTAGTAAATACACAGAGCAGAATTTCACAGAT 2372
GGCAAAAAAATTAAAGATGTCCAATATATGTTGGAAAAGAGCTAACAGAGAGATCATTATTCTAAAGATTGCCAT 2451
AACCTGTATTTGATAGAATTAGATTGGTAAATACATGTATTACATACACTCTGTGTAATAGAGACTTGAGCTGGAT 2530
CTGTACTGCACTGGAGTAAGCAAGAAAATTGGAAAATTGGTAACTTTCGTTGTCAGGTTGGCAACACATAGATCATATG 2609
TCTGAGGCACAAGTGGCTGTTCATCTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGCTAT 2688
CATAAATNTTCCTATGCNGNTGAATTNGTGTGAGGTCTGTGTCGCTATCCTCAAATTATTATAGTGCT 2767
GAGATCCTCAAATAATCTCAATTCCGGAGGTTCACAAATGGACTCCTGAAGTAGACAGAGTAGTGAGGTTCATG 2846
CCTCTATAAGCTCTGACTAGCCAATGGCATCCAATTTCCTCCAAACCTCTGCAGCATCTGTTATTGCCAA 2925
GGGCTAGTTCGGTTCTGCCAGCCATTGCGTTAAAAAATATAAGTAGGATAACTGTAAACCTGCATATTGCTAA 3004
TCTATAGACACCACAGTTCTAAATTCTTGAAACCACCTTACTACTTTTAAACTTAACTCAGTTCTAAATACTT 3083
GTCTGGAGCACAAACAATAAAAGGTTATCTTATAGTTGACTTTAACTTTGAGACCACAATTCACTTTAGTT 3162
TTCTTTACTTAAATCCATCTGCAGTCTCAAATTAAAGTTCTCCCAGTAGAGATTGAGTTGAGCCTGTATATCTATT 3241
AAAAATTCAACTCCCACATATATTACTAAGATGATTAAGACTTACATTCTGCACAGGTCTGCAAAACAAAAAT 3320
TATAAAACTAGTCCATCCAAGAACCAAAGTTGTATAAACAGGTTGCTATAAGCTGGTGAAATGAAACATTTC 3399
AATCAAACATTCCCTATATAACAATTATTATTTACAATTGGTTCTGCAATTTCCTATGTCCACCCCTTTAA 3478
AAATTATTATTGAAGTAATTATTACAGGAAATGTTAATGAGATGTATTCTTATAGAGATATTCTACAGAAAG 3557
CTTTGTAGCAGAATATATTGCAGCTATTGACTTGTAAATTAGGAAAATGTATAAGATAAAATCTATTAAATT 3636
TTCTCCTCTAAAAACTGAAAAAAAAAAAAAGGGCGGCCGC 3687

Figure 5A

FGTCGACCCACCGCTCGCTGGCAGCCCAGCTACCGTGTGACCAGATCCAGCTTGCAGCTAGCTTGTTCATTC 79

M	Q	R	L	G	G	I	L	L	C	T	L	12								
GAATTGGGCGGCCAGCGCGGAACAAAC	ATG	CAG	CGG	CTC	GGG	GGT	ATT	TTG	CTG	TGT	ACA	CTG	145							
L	A	A	A	V	P	T	A	P	S	P	T	V	T	W	T	P	A	32		
CTG	GCG	GCG	GCG	GTC	CCC	ACT	GCT	CCT	GCT	CCT	TCC	CCG	ACG	GTC	ACT	TGG	ACT	CCG	GCG	205
E	P	G	P	A	L	N	Y	P	Q	E	E	A	T	L	N	E	M	F	R	52
GAG	CCG	GGC	CCA	GCT	CTC	AAC	TAC	CCT	CAG	GAG	GAA	GCT	ACG	CTC	AAT	GAG	ATG	TTT	CGA	265
E	V	E	E	L	M	E	D	T	Q	H	K	L	R	S	A	V	E	E	M	72
GAG	GTG	GAG	GAG	CTG	ATG	GAA	GAC	ACT	CAG	CAC	AAA	CTG	CGC	AGT	GCC	GTG	GAG	GAG	ATG	325
E	A	E	E	A	A	A	K	T	S	S	E	V	N	L	A	S	L	P	P	92
GAG	GCG	GAA	GAA	GCA	GCT	GCT	AAA	ACG	TCC	TCT	GAG	GTG	AAC	CTG	GCA	AGC	TTA	CCT	CCC	385
N	Y	H	N	E	T	S	T	E	T	R	V	G	N	N	T	V	H	V	H	112
AAC	TAT	CAC	AAT	GAG	ACC	AGC	ACG	GAG	ACC	AGG	GTG	GGA	AAT	AAC	ACA	GTC	CAT	GTG	CAC	445
Q	E	V	H	K	I	T	N	N	Q	S	G	Q	V	V	F	S	E	T	V	132
CAG	GAA	GTT	CAC	AAG	ATA	ACC	AAC	AAC	CAG	AGT	GGA	CAG	GTG	GTC	TTT	TCT	GAG	ACA	GTC	505
I	T	S	V	G	D	E	E	G	K	R	S	H	E	C	I	I	D	E	D	152
ATT	ACA	TCT	GTA	GGG	GAT	GAA	GAA	GGC	AAG	AGG	AGC	CAT	GAA	TGT	ATC	ATT	GAT	GAA	GAC	565
C	G	P	T	R	Y	C	Q	F	S	S	F	K	Y	T	C	Q	P	C	R	172
TGT	GGG	CCC	ACC	AGG	TAC	TGC	CAG	TTC	TCC	AGC	TTC	AAG	TAC	ACC	TGC	CAG	CCA	TGC	CGG	625
D	Q	Q	M	L	C	T	R	D	S	E	C	C	G	D	Q	L	C	A	W	192
GAC	CAG	CAG	ATG	CTA	TGC	ACC	CGA	GAC	AGT	GAG	TGC	TGT	GGG	GAC	CAG	CTG	TGT	GCC	TGG	685
G	H	C	T	Q	K	A	T	K	G	G	N	G	T	I	C	D	N	Q	R	212
GGT	CAC	TGC	ACC	CAA	AAG	GCC	ACC	AAA	GGT	GGC	AAT	GGG	ACC	ATC	TGT	GAC	AAC	CAG	AGG	745
D	C	Q	P	G	L	C	C	A	F	Q	R	G	L	L	F	P	V	C	T	232
GAT	TGC	CAG	CCT	GGC	CTG	TGT	TGT	GCC	TTC	CAA	AGA	GGC	CTG	CTG	TTC	CCC	GTG	TGC	ACA	805
P	L	P	V	E	G	E	L	C	H	D	P	T	S	Q	L	L	D	L	I	252
CCC	CTG	CCC	GTG	GAG	GGA	GAG	CTC	TGC	CAT	GAC	CCC	ACC	AGC	CAG	CTG	CTG	GAT	CTC	ATC	865
T	W	E	L	E	P	E	G	A	L	D	R	C	P	C	A	S	G	L	L	272
ACC	TGG	GAA	CTG	GAG	CCT	GAA	GGG	GCT	TTG	GAC	CGA	TGC	CCC	TGC	GCC	AGT	GGC	CTC	CTA	925
C	Q	P	H	S	H	S	L	V	Y	M	C	K	P	A	F	V	G	S	H	292
TGC	CAG	CCA	CAC	AGC	CAC	AGT	CTG	GTG	TAC	ATG	TGC	AAG	CCA	GCC	TTC	GTG	GGC	AGC	CAT	985
D	H	S	E	E	S	Q	L	P	R	E	A	P	D	E	Y	E	D	V	G	312
GAC	CAC	AGT	GAG	GAG	AGC	CAG	CTG	CCC	AGG	GAG	GCC	CCG	GAT	GAG	TAC	GAA	GAT	GTT	GGC	1045
F	I	G	E	V	R	Q	E	L	E	D	L	E	R	S	L	A	Q	E	M	332
TTC	ATA	GGG	GAA	GTG	CGC	CAG	GAG	CTG	GAA	GAC	CTG	GAG	CGG	AGC	CTA	GCC	CAG	GAG	ATG	1105

Figure 5B

A F E G P A P V E S L G G E E E I *	350
GCA TTT GAG GGG CCT GCC CCT GTG GAG TCA CTA GGC GGA GAG GAG GAG ATT TAG	1159
GCCCCAGACCCAGCTGAGTCACTGGTAGATGTGCAATAGAAATGGCTAATTTATTTCCCAGGAGTGTCCCCAAGTGTGG	1238
AATGGCCGCACTCCTTCCCAGTAGCTTCTGGCTTGACAAGGTACAGTGCAGTACATTCTCCAGGCCCTG	1317
CTTCTCTGACTTGGAAAGACAGGCATGGCGGTAAAGGGCAGCGGTAGTCGTCCTCGTGTGCTAGAAACGCTGTC	1396
TTGTTCTTCATGGATGGAAGATTGTTGAAGGGAGAGGGATGGGAAGGGGTGAAGTCTGCTCATGATGGATTGGGGGA	1475
TACAGGGAGGGAGGATGCCCTGCCTGCAGACGTGGACTTGGCAAATGTAACCTTGCTTTGTCTTGCAGCCGCTCCAT	1554
GGGCTGAGGCAGTGGCTACACAAGAGCTATGCTGCTCTGGCCCTCCACATATTCCCTGTGTTCAGCTCCTACC	1633
TCACTGTCAGCACAGCCCTCATGCCACGCCCCCTCTGCTCACCAAGCCTAGGAGGGACCAGAGGGACTTCTCT	1712
CAGAGCCCCATGCTCTCTCAACCCATACCAAGCCTCTGTGCCAGCGACAGTCCTTCAAATGGAGGGAGTGAAAT	1791
CCTTTGGTTAATTATTTCTCCTCAAGGCACGCCTGCCACTAAGGTCAAGGCTGACTTGCATGTCCTCTAACGTTCG	1870
TAGCAGTGTGGTGGACACTGTCTCCACCGACTGCTCAATACCTCTGAAAGCCAGTGCTGGAGTGCAGTCGTGAA	1949
ATTAATTGCAAGGAAGTATACTTGGCTAATTGTAGGGCTAGGATTGTGAATGAAATTGCAAAGTCGTTAGCAACAAAT	2028
GGAAAGCCTTCTCAGTCACACCGAGAAGTCACAACCAAGCCAGGTTGTAGAGTACAGCTGTGACATACAGACAGAA	2107
GAAGGCTGGCTGGATGTCAGGCCTCAGATGACGGTTCAGGTGCCAGGAACATTACCAATTCTGTATCTATCCAGAGT	2186
TATTAAAATTGAAAGTTGCACACATTGTATAAGCATGCCTTCTCCTGAGTTAAATTATGTATACACAAACATG	2265
TGGCCCTCAAAGATCATGCACAAACCACTACTCTTGCTAATTCTGGACTTTCTCTTGAATTTCATAAAATACAAA	2344
TCCCCCTTCATGCAAAAGGGCGGGCCGC	2381

Figure 6

<pre> 1 hdkk-1 ----- mdkk-1 ----- xdkk-1 ----- hdkk-2 ----- hdkk-3 <u>MORLGATLLC</u> LLLAAAVPTA PAPAP..... TATSAPV KPGPALSYPQ EEATLNEMFR mdkk-3 <u>MORLGGILLC</u> TLLAAAVPTA PAPSP..... TVTWTPA EPGPALNYPQ EEATLNEMFR cdkk-3 ----- MRRG EGPAPRRRWL LLLAVLAALC CAAAGSGGRRAASLGEMLR hdkk-4 ----- </pre>	60 -MMAL -MMVV
<pre> 61 hdkk-1 <u>GAAGATRVFV</u> AMVAAALGGH PLL...G..V SATLNSVL.. NSNAIKNLP. PPLGGAAGHP mdkk-1 CAPAAVRFLA VFTMMALCSL PLL...G..A SATLNSVL. NSNAIKNLP. PPLGGAGGQP xdkk-1 ----- ~MGSNMFPV PLIVFWGFIL DGALGFVMMT NSNSIKNVA APAGQPIGY. hdkk-2 ----- MA ALMRSKDSSC CLLLIAAVLM .. VESSOIG SSRAKLNSTK SSLGGET..P hdkk-3 EVEELMEDTO HKLRSAVEEM E.AEEAAAAKA SSEVNLANLP PSYHNENTND TKVGNNTIHV mdkk-3 EVEELMEDTO HKLRSAVEEM E.AEEAAAKT SSEVNLASLP PNYHNETSTE TRVGNNTVHV cdkk-3 EVEALMEDTO HKLRNAVQEM E.AEEEGAKK LSEVNENLP PTYHNESENTE TRIGNKTVQT hdkk-4 ----- </pre>	120 ----- -MVAAVLLGL
<pre> 121 hdkk-1 GSAV....SA APGILYPG.. .GNKYQTIDN YQPYPCAEDE ECGTDEYCAS PTRG..GDAG mdkk-1 GSAV....SV APGVLYEG.. .GNKYQTLDN YQPYPCAEDE ECGSDEYCS PSRGAAVGG xdkk-1 .YPV....SV SPDSLYDI.. .ANKYQLDA YPLYSCTEDD DCALDEFCHS SRNGNS... hdkk-2 GQAA....NR SAG.MYQGLA FGGSKKGKNL QOAYPCSSDK ECEVGRYCHS PHQGSSA... hdkk-3 HREIHKITNN QTGQMVFSET VITSGVDEEG RRSHECIIDE DCGPSMYC... .QFASF mdkk-3 HQEVHKITNN QSGQVVFSET VITSGVDEEG KRSHECIIDE DCGPTRYC... .QFSSF cdkk-3 HQEIDKVTDN RTGSTIFSET IITSIKGGEN KRNEHECIIDE DCETGKYC... .QFSTF hdkk-4 SWLC....SP LGALVLDFNN IRSSADLHGA RKGSQCLSDT DCNTRKFCLQ PRDEKP.... </pre>	180
<pre> 181 hdkk-1 VOICLACRKR RKRCMRHAMC CPGNYCKNGI QVS.. SDQNH F..RGEIEET ITESFGN.DH mdkk-1 VOICLACRKR RKRCMTHAMC CPGNYCKNGI CMP.. SDHSH FP.RGEIEES IIENLGN.DH xdkk-1 .LVCLACRKR RKRCLRDAMC CTGNYCSNGI CVPVEQDQER FQHQGLEET ILENYNNAHDH hdkk-2 ...CMVCRRK KKRCHRDGMC CPSTRCNNGI QIPV.TESIL TPHIPALDGT RHRD.RNHGH hdkk-3 QYTQCPCRGQ RMLCTRDSEC CGDQLCVWGH CTQKAT... mdkk-3 KYTCQPCRDQ QMLCTRDSEC CGDQLCAWGH CTQKAT... cdkk-3 EYKCQPCRTQ HTHCSRDVEC CGDQLCVWGE CRKATS... hdkk-4 .FCATCRGL RRRCORDAMC CPGTLCVNDV CTTME.DATP ILERQLDEQD GTHAEGTTGH </pre>	240
<pre> 241 hdkk-1 STL..DGYSR RTTLSSKMYH TKGQEGSVCL RSSDCASGLCC CAT RHFWSK ICKPVLKEGO mdkk-1 NAAAGDGYPR RTTLTSKIYH TKGQEGSVCL RSSDCAAGLCC CAT RHFWSK ICKPVLKEGO xdkk-1 ATM..DTHSK LTTSPSGMOP FKGRGDVCL RSTDCAPGLCC CAT RHFWSK ICKPVLDEGO hdkk-2 YSNHDLGWQN LGRPHTKMSH IKGHEGDGLC RSSDCTEGFCC CAT RHEWTK ICKPVLHGE hdkk-3 RGSNGTICD NORDCQPGLCC CAFORGLLFP VCTPLPVEGE mdkk-3 KGGNGTICD NORDCQPGLCC CAFORGLLPP VCTPLPVEGE cdkk-3 RGENGTCE NOHDCNPGTCC CAFOKELLFP VCTPLPVEGE hdkk-4 PV..QENQPK RKPSIKKSQG RKGQEEGLCC RTFDCCPGLCC CAT RHFWTK ICKPVLKEGO </pre>	300
<pre> 301 hdkk-1 VC TKHRR KG SHGLE IFORCYCGE GLSCRIOK D HHOASNSSRL HTCORH- mdkk-1 VC TKHRR KG SHGLE IFORCYCGE GLACRIOK D HHOASNSSRL HTCORH- xdkk-1 VC TKHRR KG SHGLE IFORCHCGA GLSCRLQGE EITVPKTSRL HTCORH- hdkk-2 VC TKORK KG SHGLE IFORCDCAK GLSCKVWKD ATVSSKARL HVCOKT hdkk-3 LCHDPASRLL DLITWELEPD GALDRCPCAS GLLCQPHSHSLVVVKPTE VGSRDQDGE. mdkk-3 LCHDPTSQLL DLITWELEPE GALDRCPCAS GLLCQPHSHSLVVMKPAF VGSHDHSEE. cdkk-3 PCHDPSNRLL NLITWELEPD GVLERCPCAS GLICQPQSSHS STTSVQELSSS NETRKNEKED hdkk-4 VC SRRGH KDTAQAPE IFORCDCGP GLLCRSQLTSS NRQH ARL RVCOKIEKL- </pre>	360
<pre> 361 hdkk-1 ----- mdkk-1 ----- xdkk-1 ----- hdkk-2 ----- hdkk-3 ILLPREVPDE YEVGSMEEV RQELEDLERS LTEEMALGEP AAAAALLGGEEI- mdkk-3 SQLPREAPDE YEDVCFIGEV RQELEDLERS LAQEMAFEGP APVES..LGGEEI- cdkk-3 PLNMDEMPFI SLIPRDILSD YEESSVIQEV RKELESLE.. DQAGVKSEH DPAHDLFLGDEI-- hdkk-4 ----- </pre>	424

Figure 7

CTCGAGGCCAAATCGGCACGAGGCCGGCTGTGGTCTAGCATAAAGCGGAGCCCAGAAGAAGGGGCGGGGT	ATG	M	1
G E A S P P A P A R R H L L V L L L L L L		21	
GGA GAA GCC TCC CCA CCT GCC CCC GCA AGG CGG CAT CTG CTG GTC CTG CTG CTG CTC CTC		137	
S T L V I P S A A A P I H D A D A Q E S		41	
TCT ACC CTG GTG ATC CCC TCC GCT GCA GCT CCT ATC CAT GAT GCT GAC GCC CAA GAG AGC		197	
S L G L T G L Q S L L Q G F S R L F L K		61	
TCC TTG GGT CTC ACA GGC CTC CAG AGC CTA CTC CAA GGC TTC AGC CGA CTT TTC CTG AAA		257	
G N L L R G I D S L F S A P M D F R G L		81	
GGT AAC CTG CTT CGG GGC ATA GAC AGC TTA TTC TCT GCC CCC ATG GAC TTC CGG GGC CTC		317	
P G N Y H K E E N Q E H Q L G N N T L S		101	
CCT GGG AAC TAC CAC AAA GAG GAG AAC CAG GAG CAC CAG CTG GGG AAC AAC ACC CTC TCC		377	
S H L Q I D K M T D N K T G E V L I S E		121	
AGC CAC CTC CAG ATC GAC AAG ATG ACC GAC AAC AAG ACA GGA GAG GTG CTG ATC TCC GAG		437	
N V V A S I Q P A E G S F E G D L K V P		141	
AAT GTG GTG GCA TCC ATT CAA CCA GCG GAG GGG AGC TTC GAG GGT GAT TTG AAG GTA CCC		497	
R M E E K E A L V P I Q K A T D S F H T		161	
AGG ATG GAG GAG AAG GAG GCC CTG GTA CCC ATC CAG AAG GAC ACG AGC TTC CAC ACA		557	
E L H P R V A F W I I K L P R R R S H Q		181	
GAA CTC CAT CCC CGG GTG GCC TTC TGG ATC ATT AAG CTG CCA CGG CGG AGG TCC CAC CAG		617	
D A L E G G H W L S E K R H R L Q A I R		201	
GAT GCC CTG GAG GGC GGC CAC TGG CTC AGC GAG AAG CGA CAC CGC CTG CAG GCC ATC CGG		677	
D G L R K G T H K D V L E E G T E S S S		221	
GAT GGA CTC CGC AAG GGG ACC CAC AAG GAC GTC CTA GAA GAG GGG ACC GAG AGC TCC TCC		737	
H S R L S P R K T H L L Y I L R P S R Q		241	
CAC TCC AGG CTG TCC CCC CGA AAG ACC CAC TTA CTG TAC ATC CTC AGG CCC TCT CGG CAG		797	
L *		243	
CTG TAG		803	
GGGTGGGGACCGGGAGCACCTGCCTGTAGCCCCCATCAGACCCTGCCCAAGCACCATAATGGAAATAAGTTCTTCT		882	
TACATCTAAAAAAAAAAAAAAAATGGCGGCCGC		928	

Figure 8

Figure 9

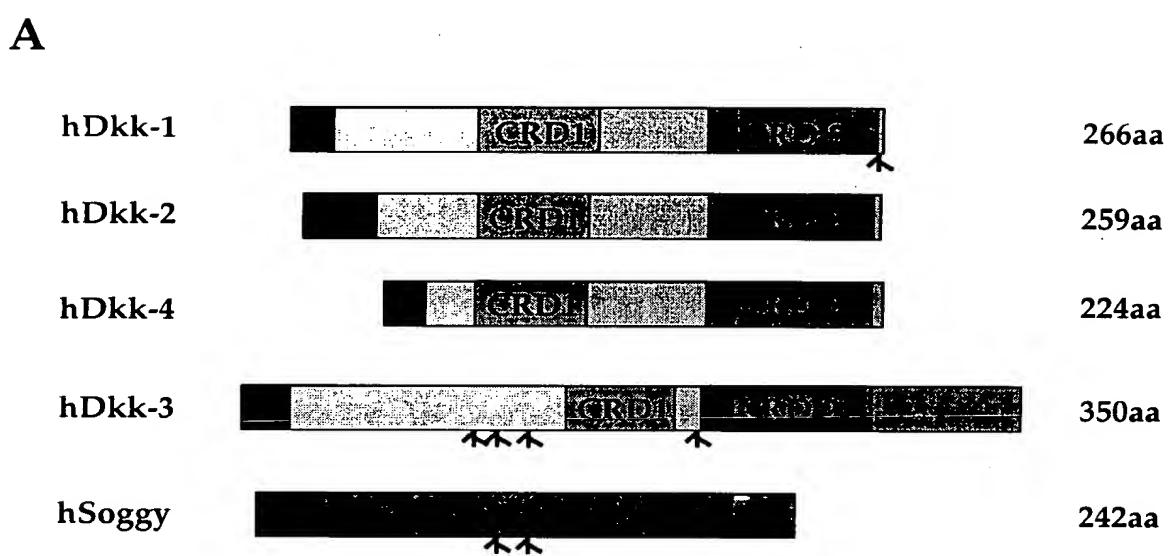


Figure 10

hsoggy	1	60
msoggy	<u>MGEASPPAPA RRHL .LVLLL LLSTLVI PSA AAPIHDADAO</u>	<u>ESSLG..... LTGLQSL</u>
hdkk-3	<u>----- MCRL .RVLLL LLPLAFVSSS ALPIHDVDSQ</u>	<u>QNTSG..... FLGLQRL</u>
mdkk-3	<u>----- MORLGATLLC LLLAAAVPTA PAPAPTATSA</u>	<u>PVKPGPALSY PQEEATLNEM</u>
	<u>----- MORLGGILLC TLLAAAVPTA PAPSPTVTWT</u>	<u>PAEPGPALNY PQEEATLNEM</u>
	*	*
hsoggy	61	120
msoggy	LQGFSRLF.. LKGNNLLRGID SL..... FSAPMDFRGL PGNYHKEENQ EHQLGNNTLS	
hdkk-3	LQSFSRLF.. LKNNDLLRDLD NF..... FSSPMDFRDL PRNFHQEENQ EHRMGNHTLS	
mdkk-3	FREVEELMED TOHKLRSAVE EMEAEAAA AK ASSEVNLANL PPSYHNETNT DTKVGNNTIH	
	FREVEELMED TQHKLRSAVE EMEAEAAA AK TSSEVNLASL PPNYHNETST ETRVGNNTVH	
	*	*
	*	*
	*	*
	*	*
	*	*
hsoggy	121	180
msoggy	SHLQIDKMTD NKTGEVLISE NVVASIQPAE GSFEGLKVP RMEEKEALVP IQKATDSFHT	
hdkk-3	SHLQIDKVTD NQTGEVHISE KVEASIEP.E RNPEGDWKVP KVEAKEPVP VQKVTDSSLHP	
mdkk-3	VHREIHKITN NQTGQMVFSE TVITSGDEE GR..... RSHECII. DEDCGP	
	VHQEVHKITN NQSGQVVFSE TVITSGDEE GK..... RSHECII. DEDCGP	
	*	*
	*	*
	*	*
	*	*
	*	*
hsoggy	181	240
msoggy	ELHPR.VAFW IIKLPRRRSH . QDALEG GHWLSEKRHR LQAIRDGLRK .. GTBKD	
hdkk-3	E.. PRQVAFW IMKMPRRRTQ . PDVQDG GRWLIEKRHR MQAIRDGLRG .. GAPERD	
mdkk-3	SMYCQFASFQ YTCQPCRGRQR MLCTRDSSECC GDQLCVWGHC TKMATRGNSG TICCDNORDCO	
	TRYCQFSSFK YTCQPCRDRQQ MLCTRDSSECC GDQLCAWGHC TQKATKGGNG TICCDNORDCO	
	*	*
	*	*
	*	*
	*	*
	*	*
hsoggy	241	300
msoggy	[REDACTED]	
hdkk-3	[REDACTED]	
mdkk-3	[REDACTED]	
	*	*
	*	*
	*	*
	*	*
	*	*
hdkk-3	301	360
mdkk-3	[REDACTED]	
	*	*
	*	*
	*	*
	*	*
hdkk-3	361	379
mdkk-3	ALGEPAAAAA ALLGEEEI-	
	APEGPAPVES .. LGGEEEI	

Figure 11

Figure 12

